

SEQUENCE ALIGNMENT -

SEQ ID NO: 2 VS. SEQ ID NO: 4

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 11:48:53 ; Search time 1 Seconds
(without alignments)
4.471 Million cell updates/sec

Title: us-10-090-516-4
Perfect score: 8858
Sequence: 1 MDVKERKPYRSLTRRRDAER.....ITDNNNGNMVNVRDSTGMPL 1624

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.0

Searched: 1 seqs, 2753 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-10-090-516-2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB Length	ID	Description
1	8858	100.0	2753	1	us-10-090-516-2	

ALIGNMENTS

RESULT 1
us-10-090-516-2

Query Match 100.0%; Score 8858; DB 1; Length 2753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDVKERKPYRSLTRRRDAERRY	TSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV	60
Db	1	MDVKERKPYRSLTRRRDAERRY	TSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV	60
Qy	61	KDIVPQEAEFCRTGANFTLRELGL	EEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD	120
Db	61	KDIVPQEAEFCRTGANFTLRELGL	EEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD	120
Qy	121	TVLSPEHPVRLWGRSTRSGRSSCL	SSRANSNLTLTDEHENTETDHPGGLQNHARLRTTP	180
Db	121	TVLSPEHPVRLWGRSTRSGRSSCL	SSRANSNLTLTDEHENTETDHPGGLQNHARLRTTP	180
Qy	181	PPLSHAHTPNQHHAAASINSLNR	GNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHAQENWL	240
Db	181	PPLSHAHTPNQHHAAASINSLNR	GNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHAQENWL	240
Qy	241	LNSNIPLETRNLGKQPFGLTLD	NLIEMDILGASRHDGAYS	300

Db 241 LNSNIPLETRNLGKQPFLGTLQDNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS 300
 Qy 301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVISATLVILLAYF 360
 Db 301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVISATLVILLAYF 360
 Qy 361 VAMHLFGLNWHLQPMEGQMYEITEDTASSWPVPTDVS LYPSGGTGLET PDRKGKGTTEGK 420
 Db 361 VAMHLFGLNWHLQPMEGQMYEITEDTASSWPVPTDVS LYPSGGTGLET PDRKGKGTTEGK 420
 Qy 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLKFNVS LGKAALVGIYG 480
 Db 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLKFNVS LGKAALVGIYG 480
 Qy 481 RKGLPPSHTQFDFVELLDGRRLLTQEARSL EGT PRQSRGT VPPSSHETGFIQYLD SGIWH 540
 Db 481 RKGLPPSHTQFDFVELLDGRRLLTQEARSL EGT PRQSRGT VPPSSHETGFIQYLD SGIWH 540
 Qy 541 LAFYNDGKESEVVSFLT TAIESVDNCPSN CYNGDCISGTCHCFLGFLGPDCGRASCPVL 600
 Db 541 LAFYNDGKESEVVSFLT TAIESVDNCPSN CYNGDCISGTCHCFLGFLGPDCGRASCPVL 600
 Qy 601 CSGNGQYMKGRCLCHSGWKGAEC DVPTNQCIDVACSNHGT CITGTICNPGYKGESCEEV 660
 Db 601 CSGNGQYMKGRCLCHSGWKGAEC DVPTNQCIDVACSNHGT CITGTICNPGYKGESCEEV 660
 Qy 661 DCM DPTCSGRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWT 720
 Db 661 DCM DPTCSGRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWT 720
 Qy 721 GHDCSIEICAADCGGHGVCVGGT CRCE DGWGAACDQ RACHPRCAEHGTCRDGKCECSPG 780
 Db 721 GHDCSIEICAADCGGHGVCVGGT CRCE DGWGAACDQ RACHPRCAEHGTCRDGKCECSPG 780
 Qy 781 WNGEHTIEGCPGLCNGNGRCTL DLNGWHCVCQLGWRGAGCDTSMETACGDSKDN DGDGL 840
 Db 781 WNGEHTIEGCPGLCNGNGRCTL DLNGWHCVCQLGWRGAGCDTSMETACGDSKDN DGDGL 840
 Qy 841 VDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLH SFYDRIKFLVGRDSTHI 900
 Db 841 VDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLH SFYDRIKFLVGRDSTHI 900
 Qy 901 IPGENPFDGGHACVIRGQVMTSDGTPLVG VNI SFVNNPLFGYTI SRQDGSFDLVTNGGIS 960
 Db 901 IPGENPFDGGHACVIRGQVMTSDGTPLVG VNI SFVNNPLFGYTI SRQDGSFDLVTNGGIS 960
 Qy 961 IILRFERAPFITQEHTLWLPWDRFFVME TIIMRHEENEIPSCDLSNFARPNPVVSPSPLT 1020
 Db 961 IILRFERAPFITQEHTLWLPWDRFFVME TIIMRHEENEIPSCDLSNFARPNPVVSPSPLT 1020
 Qy 1021 SFASSCAEKGP IVP EIQALQE EISISGCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNL M 1080
 Db 1021 SFASSCAEKGP IVP EIQALQE EISISGCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNL M 1080
 Qy 1081 KVHLMVAVEGRLFRKWFAAAPDLSYFIW DKT DVYNQKVFLSEAFVSVGYEYESCPDLI 1140
 Db 1081 KVHLMVAVEGRLFRKWFAAAPDLSYFIW DKT DVYNQKVFLSEAFVSVGYEYESCPDLI 1140
 Qy 1141 LWEKRTTVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQQPPVIGSIMGN 1200
 Db 1141 LWEKRTTVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQQPPVIGSIMGN 1200
 Qy 1201 GRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNVTNILELSHS 1260
 Db 1201 GRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNVTNILELSHS 1260
 Qy 1261 PAHKYYLATDPM SGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEVVAGTGDQCLPFDDTRC 1320
 Db 1261 PAHKYYLATDPM SGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEVVAGTGDQCLPFDDTRC 1320
 Qy 1321 GDGGKATEATLTNPRGITVDKFGLIYFVDG TMIRRIDQNGIISTLLGSNDLTSARPLSCD 1380

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Db 1321 |||||GDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCD 1380
Qy 1381 SVMDISQVHLEWPTDLAINPMDNSLYVLDNNVVLQISENHQVRIVAGRPMHCQVPGIDHF 1440
Db 1381 SVMDISQVHLEWPTDLAINPMDNSLYVLDNNVVLQISENHQVRIVAGRPMHCQVPGIDHF 1440
Qy 1441 LLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTSGEISLVAGAPSGCDCK 1500
Db 1441 LLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVTTSGEISLVAGAPSGCDCK 1500
Qy 1501 NDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRIRFIRKNKPFLNTQNM 1560
Db 1501 NDANCDCFSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNIRIRFIRKNKPFLNTQNM 1560
Qy 1561 ELSSPIDQELYLFDTTGKHLYTQSLPTGDYLYNFTYTGDGDITLITDNNGMVNVRRDST 1620
Db 1561 ELSSPIDQELYLFDTTGKHLYTQSLPTGDYLYNFTYTGDGDITLITDNNGMVNVRRDST 1620
Qy 1621 GMPL 1624
Db 1621 GMPL 1624

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Search completed: May 5, 2003, 11:48:55
Job time : 2 secs